Serial Number: 09/039,927

CRF Processing Date: 8/6/99
Edited by: _____
Verified by: _____ (STIC staff)

☐   Changed a file from non-ASCII to ASCII

☑   Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐   Edited a format error in the Current Application Data section, specifically:

ENTERED
_____

☐   Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐   Added the mandatory heading and subheadings for "Current Application Data".

☐   Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐   Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐   Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐   Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐   Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐   Inserted colons after headings/subheadings. Headings edited included:
_____

☐   Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐   Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐   Inserted mandatory headings, specifically: _____

☐   Corrected an obvious error in the response, specifically:
_____

☐   Edited identifiers where upper case is used but lower case is required, or vice versa.

☐   Corrected an error in the Number of Sequences field, specifically:
_____

☐   A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐   Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐   Other:
_____
_____
_____

*Examin r: The abov corrections must b communicated to the applicant in the first Office Action. DO NOT s nd a copy of this form.
3/1/95

┌──┐
│ **This Raw Listing contains the General** │
│ **Information Section and those Sequences** │
│ **containing ERRORS.**   │
└──┘

```
1                               SEQUENCE LISTING
2                                                           · Does Not Comply
3    (1)     General Information:                     Corrected Diskette Needed
4
5        (i) APPLICANT: Lester, Henry A.
6                      Davidson, Norman
7                      Kofuji, Paulo
8
9      (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
10           MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
11
12    (iii) NUMBER OF SEQUENCES: 2
13
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
16          (B) STREET: Four Embarcadero Center, Suite 3400
17          (C) CITY: San Francisco
18          (D) STATE: California
19          (E) COUNTRY: United States
20          (F) ZIP: 94111-4187
21
22     (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Floppy disk
24          (B) COMPUTER: IBM PC compatible
25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28     (vi) CURRENT APPLICATION DATA:
29          (A) APPLICATION NUMBER: US 09/039,927
30          (B) FILING DATE: 16-MAR-1998
31          (C) CLASSIFICATION:
32
33    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: US 08/066,371
35          (B) FILING DATE: 21-MAR-1993
36
37    (vii) PRIOR APPLICATION DATA:
38          (A) APPLICATION NUMBER: US 08/614,801
39          (B) FILING DATE: 07-MAR-1996
40
41   (viii) ATTORNEY/AGENT INFORMATION:
42          (A) NAME: Trecartin, Richard F.
43          (B) REGISTRATION NUMBER: 31,801
44          (C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
45
```

INPUT SET: S32821.raw

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46      (ix) TELECOMMUNICATION INFORMATION:
47           (A) TELEPHONE: (415) 781-1989
48           (B) TELEFAX: (415) 398-3249
49           (C) TELEX: 910 277299
50
```

ERRORED SEQUENCES FOLLOW:

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51      (2) INFORMATION FOR SEQ ID NO:1:
52
53           (i) SEQUENCE CHARACTERISTICS:
54               (A) LENGTH: 2076 base pairs
55               (B) TYPE: nucleic acid
56               (C) STRANDEDNESS: single
57               (D) TOPOLOGY: linear
58
59           (ii) MOLECULE TYPE: cDNA
60
61           (ix) FEATURE:
62               (A) NAME/KEY: CDS
63               (B) LOCATION: 32..1534
64
65           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67      GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA
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69                                         Met Ser Ala Leu Arg Arg Lys
70                                          1               5
71
72      TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC
73      100
74      Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
75              10              15              20
76
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79      Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
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81
82      AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG
83      196
84      Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
85       40              45              50              55
86
87      CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC
88      244
89      Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
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91
92      TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC
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INPUT SET: S32821.raw

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 94     Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
 95                 75                  80                  85
 96
 97     ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG
 98     340
 99     Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
100                 90                  95                 100
101
102     GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC
103     388
104     Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
105             105                 110                 115
106
107     TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT      436
108     Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
109     120             125                 130                 135
110
111     TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC
112     484
113     Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
114                 140                 145                 150
115
116     ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC
117     532
118     Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
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120
121     CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG
122     580
123     Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
124             170                 175                 180
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126     ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT
127     628
128     Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
129         185                 190                 195
130
131     GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG
132     676
133     Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val
134     200             205                 210                 215
135
136     GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG
137     724
138     Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys
139             220                 225                 230
140
141     CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC
142     772
143     Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp
144             235                 240                 245
145
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,927*

INPUT SET: S32821.raw

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152   868
153   Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro
154       265                 270                 275
155
156   TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG
157   916
158   Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val
159   280                 285                 290                 295
160
161   GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA
162   964
163   Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln
164                 300                 305                 310
165
166   GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT
167   1012
168   Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe
169               315                 320                 325
170
171   TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC
172   1060
173   Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser
174           330                 335                 340
175
176   CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA
177   1108
178   Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys
179       345                 350                 355
180
181   GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC
182   1156
183   Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala
184   360                 365                 370                 375
185
186   ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA
187   1204
188   Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly
189                 380                 385                 390
190
191   CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG
192   1252
193   Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr
194               395                 400                 405
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INPUT SET: S32821.raw

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206    ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC
207    1396
208    Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr
209    440                   445                   450                   455
210
211    ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA
212    1444
213    Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro
214                  460                   465                   470
215
216    CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT
217    1492
218    Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn
219              475                   480                   485
220
-->    221    CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA              1534
       222    Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
       223        490                   495                   500
       224
       225    TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT
-->    226    CCAATATTTG    1594
       227
       228    GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG
-->    229    GCAAATTCAT    1654
       230
       231    CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA
-->    232    AGGGAGGACA    1714
       233
       234    TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA
-->    235    ATGTGCAAAT    1774
       236
       237    TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA
-->    238    TATTCTGGAA    1834
       239
       240    AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA
-->    241    ATATATGTAT    1894
       242
       243    TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG
-->    244    CATACATACA    1954
       245
       246    TACATGCATA TGCACAGACA CATACACACA CATACTCATA TATATAAAAC
-->    247    ATACCCATAC    2014
       248
       249    AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA
-->    250    AAAAAACTCG    2074
       251
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/039,927*

INPUT SET: S32821.raw
2076

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252   AG
253
254
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/039,927*

DATE: 08/06/1999
TIME: 13:15:05

INPUT SET: S32821.raw

Line	Error	Original Text
54	Entered (2076) and Calc. Seq. Length (182) differ	(A) LENGTH: 2076 base pairs
107	# of Sequences for line conflicts w/ running total	TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC
221	# of Sequences for line conflicts w/ running total	CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GA
226	# of Sequences for line conflicts w/ running total	CCAATATTTG 1594
229	# of Sequences for line conflicts w/ running total	GCAAATTCAT 1654
232	# of Sequences for line conflicts w/ running total	AGGGAGGACA 1714
235	# of Sequences for line conflicts w/ running total	ATGTGCAAAT 1774
238	# of Sequences for line conflicts w/ running total	TATTCTGGAA 1834
241	# of Sequences for line conflicts w/ running total	ATATATGTAT 1894
244	# of Sequences for line conflicts w/ running total	CATACATACA 1954
247	# of Sequences for line conflicts w/ running total	ATACCCATAC 2014
250	# of Sequences for line conflicts w/ running total	AAAAAACTCG 2074

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,927*

DATE: 08/06/1999
TIME: 18:23:32

INPUT SET: S32821.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                    SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANT: Lester, Henry A.
 6                        Davidson, Norman
 7                        Kofuji, Paulo
 8
 9        (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
10             MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
11
12       (iii) NUMBER OF SEQUENCES: 2
13
14        (iv) CORRESPONDENCE ADDRESS:
15             (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
16             (B) STREET: Four Embarcadero Center, Suite 3400
17             (C) CITY: San Francisco
18             (D) STATE: California
19             (E) COUNTRY: United States
20             (F) ZIP: 94111-4187
21
22         (v) COMPUTER READABLE FORM:
23             (A) MEDIUM TYPE: Floppy disk
24             (B) COMPUTER: IBM PC compatible
25             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28        (vi) CURRENT APPLICATION DATA:
29             (A) APPLICATION NUMBER: US 09/039,927
30             (B) FILING DATE: 16-MAR-1998
31             (C) CLASSIFICATION:
32
33       (vii) PRIOR APPLICATION DATA:
34             (A) APPLICATION NUMBER: US 08/066,371
35             (B) FILING DATE: 21-MAR-1993
36
37       (vii) PRIOR APPLICATION DATA:
38             (A) APPLICATION NUMBER: US 08/614,801
39             (B) FILING DATE: 07-MAR-1996
40
41      (viii) ATTORNEY/AGENT INFORMATION:
42             (A) NAME: Trecartin, Richard F.
43             (B) REGISTRATION NUMBER: 31,801
44             (C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
45
46        (ix) TELECOMMUNICATION INFORMATION:
```

ENTERED

```
47          (A) TELEPHONE: (415) 781-1989
48          (B) TELEFAX: (415) 398-3249
49          (C) TELEX: 910 277299
50
51    (2) INFORMATION FOR SEQ ID NO:1:
52
53          (i) SEQUENCE CHARACTERISTICS:
54                (A) LENGTH: 2076 base pairs
55                (B) TYPE: nucleic acid
56                (C) STRANDEDNESS: single
57                (D) TOPOLOGY: linear
58
59          (ii) MOLECULE TYPE: cDNA
60
61          (ix) FEATURE:
62                (A) NAME/KEY: CDS
63                (B) LOCATION: 32..1534
64
65          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67    GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA      52
68                                      Met Ser Ala Leu Arg Arg Lys
69                                        1               5
70
71    TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC   100
72    Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
73             10              15               20
74
75    TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC   148
76    Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
77         25              30              35
78
79    AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG   196
80    Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
81     40              45              50                      55
82
83    CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC   244
84    Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
85                 60                  65                  70
86
87    TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC   292
88    Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
89                 75                  80                  85
90
91    ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG   340
92    Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
93             90                  95                  100
94
95    GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC   388
96    Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
97         105                 110                 115
98
99    TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT   436
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,927*

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104    Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
105                    140                 145             150
106
107    ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC    532
108    Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
109            155                 160             165
110
111    CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG    580
112    Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
113            170                 175             180
114
115    ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT    628
116    Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
117        185                 190             195
118
119    GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG    676
120    Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val
121    200             205                 210             215
122
123    GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG    724
124    Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys
125                    220                 225             230
126
127    CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC    772
128    Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp
129            235                 240             245
130
131    CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT    820
132    Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe
133            250                 255                 260
134
135    CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC    868
136    Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro
137        265                 270                 275
138
139    TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG    916
140    Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val
141    280             285                 290             295
142
143    GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA    964
144    Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln
145                    300                 305             310
146
147    GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT    1012
148    Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe
149            315                 320             325
150
151    TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC    1060
152    Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,927*

INPUT SET: S32821.raw

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157        345                  350                   355
158
159    GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC   1156
160    Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala
161    360                  365                   370                   375
162
163    ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA   1204
164    Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly
165                 380                  385                   390
166
167    CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG   1252
168    Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr
169                 395                  400                   405
170
171    GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT   1300
172    Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr
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174
175    TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA   1348
176    Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg
177        425                  430                   435
178
179    ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC   1396
180    Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr
181    440                  445                   450                   455
182
183    ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA   1444
184    Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro
185                 460                  465                   470
186
187    CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT   1492
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191    CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA          1534
192    Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
193        490                  495                   500
194
195    TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG   1594
196
197    GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT   1654
198
199    CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA   1714
200
201    TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT   1774
202
203    TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA   1834
204
205    AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT   1894
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206
207   TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACATACA   1954
208
209   TACATGCATA TGCACAGACA CATACACACA CATACTCATA TATATAAAAC ATACCCATAC   2014
210
211   AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAACTCG   2074
212
213   AG                                                                2076
214
215
216   (2) INFORMATION FOR SEQ ID NO:2:
217
218        (i) SEQUENCE CHARACTERISTICS:
219             (A) LENGTH: 501 amino acids
220             (B) TYPE: amino acid
221             (D) TOPOLOGY: linear
222
223        (ii) MOLECULE TYPE: protein
224
225        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
226
227   Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr
228    1               5                  10                  15
229
230   Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
231             20                  25                  30
232
233   Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
234         35                  40                  45
235
236   Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
237       50                  55                  60
238
239   Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
240    65                  70                  75                  80
241
242   Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
243             85                  90                  95
244
245   Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
246             100                 105                 110
247
248   Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr
249         115                 120                 125
250
251
252   Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile
253         130                 135                 140
254
255   Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile
256    145                 150                 155                 160
257
258   Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
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****** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

```
51   (2) INFORMATION FOR SEQ ID NO:1:
52
53       (i) SEQUENCE CHARACTERISTICS:
54           (A) LENGTH: 2076 base pairs
55           (B) TYPE: nucleic acid
56           (C) STRANDEDNESS: single
57           (D) TOPOLOGY: linear
58
59       (ii) MOLECULE TYPE: cDNA
60
61       (ix) FEATURE:
62           (A) NAME/KEY: CDS
63           (B) LOCATION: 32..1534
64
65       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67   GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA    52
68                                     Met Ser Ala Leu Arg Arg Lys
69                                      1               5
70
71   TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC   100
72   Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
73           10              15                  20
74
75   TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC   148
76   Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
77       25              30                  35
78
79   AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG   196
80   Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
81   40              45                  50                      55
82
83   CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC   244
84   Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
85                   60                  65                  70
86
87   TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC   292
88   Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
89                   75                  80                  85
90
91   ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG   340
92   Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
93           90                  95                  100
94
95   GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC   388
96   Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
97       105                 110                 115
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INPUT SET: S32821.raw

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 98
 99   TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT   436
100   Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
101   120             125             130                 135
102
103   TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC   484
104   Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
105                   140             145                 150
106
107   ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC   532
108   Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
109           155             160             165
110
111   CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG   580
112   Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
113           170             175             180
114
115   ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT   628
116   Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
117       185             190             195
118
119   GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG   676
120   Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val
121   200             205             210                 215
122
123   GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG   724
124   Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys
125           220             225             230
126
127   CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC   772
128   Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp
129           235             240             245
130
131   CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT   820
132   Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe
133           250             255             260
134
135   CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC   868
136   Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro
137       265             270             275
138
139   TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG   916
140   Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val
141   280             285             290                 295
142
143   GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA   964
144   Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln
145               300             305             310
146
147   GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT  1012
148   Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe
149           315             320             325
150
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INPUT SET: S32821.raw

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151   TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC   1060
152   Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser
153           330                 335                 340
154
155   CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA   1108
156   Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys
157           345                 350                 355
158
159   GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC   1156
160   Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala
161   360                 365                 370                 375
162
163   ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA   1204
164   Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly
165               380                 385                 390
166
167   CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG   1252
168   Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr
169           395                 400                 405
170
171   GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT   1300
172   Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr
173           410                 415                 420
174
175   TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA   1348
176   Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg
177           425                 430                 435
178
179   ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC   1396
180   Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr
181   440                 445                 450                 455
182
183   ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA   1444
184   Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro
185               460                 465                 470
186
187   CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT   1492
188   Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn
189               475                 480                 485
190
191   CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA           1534
192   Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
193               490                 495                 500
194
195   TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG   1594
196
197   GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT   1654
198
199   CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA   1714
200
201   TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT   1774
202
203   TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA   1834
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INPUT SET: S32821.raw

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204
205   AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT    1894
206
207   TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACATACA    1954
208
209   TACATGCATA TGCACAGACA CATACACACA CATACTCATA TATATAAAAC ATACCCATAC    2014
210
211   AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAACTCG    2074
212
213   AG                                                                 2076
214
215
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/039,927*

INPUT SET: S32821.raw

Line   Error   Original Text